

Query Match	100.0%	Score 4928	DB 18	Length 919
FT	Modified-site	798	/label= autophosphorylation_site	
FT			/note= "putative"	
FT	Binding-site	844..847	/label= binding_motif_for_p13_kinase	
FT			/note= "binding motif for phosphatidylinositol 3' kinase"	
FT	Binding-site	832..832	/label= potential_substrate_binding_site	
FT	Binding-site	506..509	/label= putative_receptor_binding_site_for_SHC	
FT			/note= "SHC is an oncogenic SH2 domain containing molecule"	
FT	Binding-site	510..513	/label= GTPase_activity-protein_binding_site	
FT			/note= "putative"	
FT	Region	505..541	/note= "alternatively spliced variant"	
FT	Region	666..671	/note= "alternatively spliced sequence"	
FT	Region	26..42	/note= "antibody recognition sequence N1alpha"	
FT	Region	309..321	/note= "antibody recognition sequence N1beta"	
FT	Region	902..919	/note= "antibody recognition sequence C1beta"	
PN	US5677144-A.			
PD	14-OCT-1997.			
PF	08-NOV-1994.	94US-036343.		
PR	16-NOV-1993.	93US-015397.		
PA	(ALIVE/) ALVES F H E.			
PA	(ULIK/) ULLRICH A.			
PI	Alves FHE, Ullrich A;			
PI	WPI; 1997-511869/47.			
DR	N-PDB; AAT93785.			
PT	Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding			
PT	for it, useful for cancer diagnosis			
PS	Disclosure; Fig 1; 70pp; English.			
XX	The present sequence represents the protein sequence of a mammary carcinoma kinase, called MCK-10. This kinase belongs to a novel family of receptor tyrosine kinases, and expression is associated with proliferative diseases such as cancer. The MCK-10 receptor tyrosine kinase has extensive sequence similarity to the insulin receptor family. The MCK-10 gene was isolated by PCR using 2 degenerate oligonucleotide primer pools, using a template cDNA synthesised by reverse transcription of poly-A RNA from the human mammary carcinoma cell line MCF7. The MCK-10 protein contains 2 alternative spliced sequences, from amino acids 505-541 and 666-671. The sequence represented by amino acids 585-595 may be important, as deletion of this motif in the activin receptor kinase/threonine kinase results in reduced ligand binding affinity. The tyrosine kinase neurotrophin receptor. Modulation of MCK-10 activity therefore may be used for treatment of neurological disorders. MCK-10 is also expressed in a variety of cancer cell lines and tumour tissue. The nucleotide sequence of MCK-10, or parts of it, can be used for diagnostic purposes to detect aberrant expression of MCK-10 genes. Inhibitors of MCK-10 receptor activity may have therapeutic value in the treatment of diseases such as cancer.			
XX	Sequence	919 AA.		

	Best Local Similarity	100.0%	Pred. No. 0;	Matches 919;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGPEALSSLLLLLLVLAASGDADMKGHFDPKACRYALAGMDRITPPDSIDISASSWSNSTAAR	60					
Db	1	mppealssllllllvasgdadmkghfdpkacryalgmdrttppdsidisasswsnstaar	60					
QY	61	HSRLSSDGDGAWCPAGSYFPEKEEYLQVDLORLHLVALVTOGRHAGLGKEFSRYRL	120					
Db	61	hsrlssdgdgawcpagsvfpekeeylqvdlqrlhlvalvsgqghagglgkefsryrl	120					
QY	121	RFSRPGRRMGKDKRMGQGVISGNDPEGVYKLDGPPVAVRLVFPYPRADRVMSCLRV	180					
Db	121	rfsrgrrmgkdxwgqvgvlsgnepegvylkdgppvavrlvfypradrvmsvclrv	180					
QY	181	ELYGCLMRDGLSLYAPVQOTWLYLSEAVVLLNDSTYDGHVTGGLQYQGLQDLADVYVGLDD	240					
Db	181	elygclmrldgsllytapvqotwmylseavvllndstygthvvgllqyqglqdladvvgldd	240					
QY	241	EKRSQELRWPQYDYVGVGNHSFSSGYVMEEPDRIRAFQAMQVHCNNMHTLGARLGG	300					
Db	241	ekrsqelrwpdydyvgvgnhsfssgyvemeefdrlafqamqvhcnmhtlgarlgg	300					
QY	301	VECRFRRGFAMWEGEPKRNHLGMLGPRARAVSVPLGGRVARELQCRFTLPGFWLFS	360					
Db	301	vecfrrrgamewegemphnlgmlgpraravsvplgrarvrlqcrftlpgfwllfs	360					
QY	361	EISFISDYVNNSSPALGCTFPAPMWPPEPPPTNSSLELPRGQOPVAKAAGSTPALLI	420					
Db	361	eisfisdvnnsspalgctfppapwppppptnsslelprgqpvakaaegstalll	420					
QY	421	GCLVALILLLLLLIILMLRLHMRRLLSAERRYVEELTVLSPGQDITLNNBPGRPE	480					
Db	421	gclvalilllllllilmlrlhmrlllsaeerrveeltvhlspgdtllnnbpgrpe	480					
QY	481	PPPYQDPFRPGRNPBSAPCVNGSALLNSNPAIRYLLATYARPPRGCPPTPAMAKPTNT	540					
Db	481	pppyqdpfrpgrnpbsapcvngsalllnspayrlllatyarprrgpprpawakpnt	540					
QY	541	QAYSQGYMEPEKRGAPLILPPRPONGSVPHAEADIVTLQVGNQYAVPALPBGAVGDP	600					
Db	541	qaysqgyમેપેકrgapllpprpqngsvphaeadivtlqvgngyavpalpbgavgdp	600					
QY	601	PRVDEPPRSRLRERKELGEGQFGEVHLCEYDSQDVLVSLDFPLNVKRGHPLVAVKILRPD	660					
Db	601	prvdfprsrllrerkelgsegqfgevhlceydsqdvlsldfplnvkrghpllvavkllrpd	660					
QY	661	ATKNAVSFLSFANDLKEVKIMSRKLDPIITLLGVCVQDDPLCMTITDMENGDINQELS	720					
Db	661	atknavsflsfandllekvkimsrlkdpillllgvcvqddplcmldymengdinqfls	720					
QY	721	AHQLEDKAEGAPGGGAAOQPTIYVPMILHVAAGIASGMRLATLNFVHRDLATRNCIV	780					
Db	721	ahqledkaegapgggaaqgplisylpmllhvaaglaagmyrlatlnfhrdlatrnciv	780					
QY	781	GENFTIKLADFGKSNRLTAGDIYRVQGRAVLPIRMMAMECIIMGFTTASDVMAFGVTLM	840					
Db	781	genftikladifmsrnllyagdyrvqgravlipirmamecilmgkftlasdvmafgvltlw	840					
QY	841	EVLMLCRAQPFQQLNDEQVITENAGEFFRDOGRQVYLSRPACPOGLYEMLTMCNRESEQ	900					
Db	841	evlmlcraqpfqqldeqylenagefftdqgrqylylsrppacpglyelmltrcwsreseq	900					
QY	901	RPPFSQLRHFLAEDALNTV 919						
Db	901	rppfsqlrhlfaedaltv 919						
AC	AAK75502							
AC	AAK75502 standard; Protein: 919 AA.							

XX 26-NOV-1995 (first entry)
 XX Human mammary carcinoma kinase 10 (MCK-10).
 DE XX
 XX Mammary carcinoma kinase 10; transmembrane receptor;
 KW receptor tyrosine kinase; cancer.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= signal
 FT Domain 31..185
 FT /label= disordered I-like domain
 FT Cleavage-site 304..307
 FT /label= putative precursor cleavage site
 FT Region 417..439
 FT /label= transmembrane
 FT MISC-difference 505..541
 FT /label= alternatively spliced sequence I
 FT MISC-difference 666..671
 FT /label= alternatively spliced sequence II
 FT MISC-difference 25..42
 FT /label= NT alpha
 FT /note= "peptide antibody recognition site"
 FT MISC-difference 309..321
 FT /label= NT beta
 FT /note= "see above"
 FT MISC-difference 909..919
 FT /label= CT beta
 FT /note= "see above"
 XX
 PN W09514088-A.
 XX
 PD 26-MAY-1995.
 XX
 PF 16-NOV-1994; 94WO-EP03797.
 XX
 PR 16-NOV-1993; 93US-0153397.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Alves FHE, Ulrich A;
 XX
 DR WPI; 1995-224054/29.
 XX
 DR N-PSDB; AA092520.
 XX
 XX New nucleic acid encoding MCK-10 receptor tyrosine kinase - and
 PT derived vectors, transformed cells, proteins and antibodies useful
 PT for diagnosis and treatment of proliferative disease, esp. cancer,
 PT and for screening modulators
 XX
 PS Disclosure; Page 53-55; 115pp; English.
 XX
 XX cDNA prep. from human breast cancer cell line MCF7 (ATCC HTB22) and
 CC used in a PCR with two degenerate oligo primer pools based on
 CC conserved sequences of the kinase domain of receptor tyrosine
 CC kinases. One clone, designated MCK-10, was identified as novel RTK.
 CC The PCR fragment was used to screen a lambda gt11 library of human
 CC fetal brain cDNA. Several overlapping clones were identified. The
 CC composite of these cDNA clones is given in AA092520 and the deduced AA
 CC sequence in AA075502. Some of the clones had a deletion of 6 AAs at
 CC posn. 2315 in the MCK-10 sequence. MCK-10 has all the
 CC characteristics of a receptor TK (see AA075502 FT). Screening of
 CC human placental library yielded two cDNA clones MCK-10-1 and
 CC MCK-10-2. One of the clones isolated from the human fetal brain
 CC library contd. an additional 18 nts in the TK domain. The MCK-10 splice
 CC isoforms have been designated MCK-10-1 (with an additional 111 bp
 CC between nts 1832 and 1943); MCK-10-2 (without any insertions); MCK-10-3
 CC (with the additional 111 bp and and 18 bp in the TK domain); and MCK10-4
 CC (with the additional 18 bp). The predicted mol. wts. of MCK-10-1 and
 CC MCK-10-2 proteopreors are 101.13 and 97.17 kD respectively, and can thus

CC be subdivided into a 34.31 kD alpha subunit and and 66.84 or 62.88 kD
 CC beta subunits that contain the TK homology and alternative splice sites.
 XX
 XX Sequence 919 AA:
 SQ
 Query Match 99.9%; Score 4921; DB 16; Length 919;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MGPEALSLILLIVASGADMKGHPDPAKCYALGMODRTIPDSISSSSSSSTAR 60
 DB 1 MGPEALSLILLIVASGADMKGHPDPAKCYALGMODRTIPDSISSSSSSSTAR 60
 QY 61 HSRLESSDGDGAWCPAGSVFPEEETLYQVLDRLHLVALYGTGHNAGGLKEFSRYRL 120
 DB 61 HSRLESSDGDGAWCPAGSVFPEEETLYQVLDRLHLVALYGTGHNAGGLKEFSRYRL 120
 QY 121 RYSGDGRMMGKKDRMGQEVISGNEDEPGVVLKDLGPPVAVRLVRFPRADRVMSCLRV 180
 DB 121 RYSGDGRMMGKKDRMGQEVISGNEDEPGVVLKDLGPPVAVRLVRFPRADRVMSCLRV 180
 QY 181 ELYGCLMRDGLSYAPVQGTMYLSEAYVLYNSTYDGHVGGLOYGGLADYVGLDD 240
 DB 181 ELYGCLMRDGLSYAPVQGTMYLSEAYVLYNSTYDGHVGGLOYGGLADYVGLDD 240
 QY 241 FRKSOELRWPGDYVYVGNMNSHSSGYYMEPEFRLRFAOMAYCNMHTLGARLGG 300
 DB 241 FRKSOELRWPGDYVYVGNMNSHSSGYYMEPEFRLRFAOMAYCNMHTLGARLGG 300
 QY 301 VECRRRRGPMAMEEPEMRHNLGNLGDPRARAVSVPLGGRVARELQCRFLFAGPMLFS 360
 DB 301 VECRRRRGPMAMEEPEMRHNLGNLGDPRARAVSVPLGGRVARELQCRFLFAGPMLFS 360
 QY 361 EISFISDVYNNSSPALGFFPPAPPMWPPGPPPTNSSLELFRGQOPPAKAGSFTALLI 420
 DB 361 EISFISDVYNNSSPALGFFPPAPPMWPPGPPPTNSSLELFRGQOPPAKAGSFTALLI 420
 QY 421 GCLVALILLILLIILMLRLHMRRLSKAEERYVEEETLYVLSVPGDTIILNNPGPRE 480
 DB 421 GCLVALILLILLIILMLRLHMRRLSKAEERYVEEETLYVLSVPGDTIILNNPGPRE 480
 QY 481 PPTQEPFRPGNPPHSAPCPVNGSALLSNPARYLLATYARPPGPPPPAMAKPNT 540
 DB 481 PPTQEPFRPGNPPHSAPCPVNGSALLSNPARYLLATYARPPGPPPPAMAKPNT 540
 QY 541 QAYSQDYMEPEKPGAPLPPPPQNSVPHYAEADYTLQGVGNTYVAPALPGAVGDP 600
 DB 541 QAYSQDYMEPEKPGAPLPPPPQNSVPHYAEADYTLQGVGNTYVAPALPGAVGDP 600
 QY 601 PRVDPFRRLRFKEKLGSGGFEVHLCEVDSFODVSLDFPLNVRKGPPLVAVKILRPD 660
 DB 601 PRVDPFRRLRFKEKLGSGGFEVHLCEVDSFODVSLDFPLNVRKGPPLVAVKILRPD 660
 QY 661 ATKNASFSLFRNDLKEVKTMSRLKDPNIRLLGVCVQDDPLCMITDYMNGDLNGLFS 720
 DB 661 ATKNASFSLFRNDLKEVKTMSRLKDPNIRLLGVCVQDDPLCMITDYMNGDLNGLFS 720
 QY 721 AHOLEDKABAPGGOAAGPTISYPLMLVANAQIASGMRYLATLNVRHDLATRNCLV 780
 DB 721 AHOLEDKABAPGGOAAGPTISYPLMLVANAQIASGMRYLATLNVRHDLATRNCLV 780
 QY 781 GENTFIKADGMSRNLTAGDYVYRQGRVAVPIRMAMECTIMKFTTASDVNAFGYTLW 840
 DB 781 GENTFIKADGMSRNLTAGDYVYRQGRVAVPIRMAMECTIMKFTTASDVNAFGYTLW 840
 QY 841 EYLMKRAQPPGQTLDEQVYNAGGFFRQGRVYLSRPPACPGGLYELMKRCSRSSEQ 900
 DB 841 EYLMKRAQPPGQTLDEQVYNAGGFFRQGRVYLSRPPACPGGLYELMKRCSRSSEQ 900
 QY 901 RPPFSOLHRLAEDALNTV 919
 DB 901 RPPFSOLHRLAEDALNTV 919

RESULT 3
 ID AAR75504 standard; Protein: 919 AA.
 XX AAR75504;
 AC AAR75504;
 XX 26-NOV-1995 (first entry)
 XX
 XX Human mammary carcinoma kinase 10 (MCK-10).
 DE
 XX Mammary carcinoma kinase 10; MCK-10; transmembrane receptor;
 KW receptor tyrosine kinase; cancer.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide 1..18
 FT /label= signal
 FT Domain 31..185
 FT /label= discolidin I-like domain
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 FT /label= NT alpha
 FT /note= "peptide antibody recognition site"
 FT MISC-difference 309..321
 FT /label= NT beta
 FT /note= "see above"
 FT MISC-difference 909..919
 FT /label= CT beta
 FT /note= "see above"
 XX
 XX W09514089-A.
 XX
 XX 26-MAY-1995.
 XX
 XX 16-NOV-1994; 94MO-EP03799.
 XX
 XX 16-NOV-1993; 93US-0153397.
 XX
 XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 XX Alves FHE, Ullrich A;
 XX
 XX WPI; 1995-224055/29.
 XX
 XX N-PSDB; AA092522.
 XX
 XX New nucleic acid encoding CCK-2 receptor tyrosine kinase - and
 PT derived vectors, transformed cells, proteins and antibodies, useful
 PT for diagnosis and treatment of proliferative and nervous system
 PT diseases and for screening modulators
 XX
 XX Disclosure: Page 70-72; 115pp; English.
 XX
 XX CDNA prep'd. from human breast cancer cell line MCF7 (ATCC HTB22) was
 CC used in a PCR with two degenerate oligo primer pools based on
 CC conserved sequences of the kinase domain of receptor tyrosine
 CC kinases. One clone, designated MCK-10, was identified as novel RTK.
 CC The PCR fragment was used to screen a lambda gtl1 library of human
 CC fetal brain cDNA. Several overlapping clones were identified. The
 CC composite of these cDNA clones is given in AA092522 and the deduced AA
 CC sequence in AAR75504. Some of the clones had a deletion of 6A at posn.
 CC 2315 in the MCK-10 sequence. MCK-10 has all the characteristics of
 CC a receptor PTK (see AAR75504 FT). Screening of human placental library
 CC yielded two cDNA clones. One of the clones isolated from the human

CC fetal brain library contained an additional 18 nts in the TK
 CC domain. The MCK-10 splice isoforms have been designated MCK-10-1
 CC (with an additional 111 bp between nts 1832 and 1943); MCK-10-2
 CC (without any insertions); MCK-10-3 (with the additional 111 bps and
 CC 18 bp in the TK domain); and MCK-10-4 (with the additional 18 bp).
 CC The predicted mol. wts. of MCK-10-1 and MCK-10-2 precursors are
 CC 101.13 and 97.17 kD respectively, and can thus be subdivided into a
 CC 34.31 kD alpha subunit and a 66.84 or 62.86 kD beta subunits that
 CC contain the TK homology and alternative splice sites.
 XX

SQ Sequence 919 AA;

Query Match 99.98; Score 4921; DB 16; Length 919;
 Best Local Similarity 99.98; Pred. No. 0;
 Matches 918; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGPALSSLLLLLVASGDADMKGFDPKACRYALGMDRTIPSDISASSMSDSTAAR 60
 DB 1 mgpalslllllllvassgdadmkgfdpakercryalgmdrtlpsdsassmsdstaar 60
 QY 61 HSRLESSDGGACWCPAGSVPFKBEETQVDLQRLHLVALVGTGRHAGGLCKEFSRYRL 120
 DB 61 hsrlessdggacwcpagsvfpkbeeylqvdlqrlhlvalvgtgrhagglckefsryrl 120
 QY 121 RYSHDGRMMGMKDRMGQEVISGNEDEGVTLKDLGPMVARLRYFPRAADRVMSVCLRY 180
 DB 121 rysdgrmmgmkdrmgqevisgndegvylkdlgppmvarlryfprradrvmsvclry 180
 QY 181 ELYGCLMRDGLSYTAVVGOTMYLSEAVYINDSTYDGHFTVGGTGLGGLADGVGLDD 240
 DB 181 elygcclmrddllytavgotmylseavyindstydhftvvggtglggladgvvgldd 240
 QY 241 FRKSQELRWVPGDYVMSKHSFSSGVEKEMFEEDRLRAFOAMQVHCNNMHTLCARLPGG 300
 DB 241 frksqelrwpvgdyvmskhsfssgyvemefedrlrafqamvchcnmhtlcarlp 300
 QY 301 VECFRFRGPAMAWEGEPHRLNLGNLGDPRARAVSVPLGGRVAREFLCRLFLPAGPWLIFS 360
 DB 301 vecfrfrgpamawegepmrhlngnlgdpraravsvplggrvarflcrlflpawpwlifs 360
 QY 361 EISFISDVVNSSPALGTFPPAPWMPGPPPTNFSSLSLEPRGOQVAKAEGSPAILI 420
 DB 361 eisfidsvvnsspalggtfppapwmpgppptnfsslsleprgqvakaegspaili 420
 QY 421 GCLVATILLLLITALLMRLMLHMRRLSKAERYLBEELTVHLSVPGDTLLINRPGPRE 480
 DB 421 gclvatillllitalmlrmlhmrllskaerylbeeltvhlsvpgdtllinnrpgpre 480
 QY 481 PPYQEPFRPGNPNPHSAPCVPNCSALLSNPARYRLILATYARPPRGPPTPAMAKPTNT 540
 DB 481 ppyqepfrpgnppnhsapcvpnpsallsnparyllilatyarpprgppcpwamakpnt 540
 QY 541 QAYSQGYMEPEKPGAPLPPPPONSVPHYAADIIVTLOGVTGNTYAVPALPPGAVDGP 600
 DB 541 qaysgyymepekpgapllpppponsvphyaaadvltvgtgntyavpalppgavdgp 600
 QY 601 PRYDFPRSRRLREFKEKGEQGFGEVHLCVDSPPDLYSLDPLVNRKGNPLVAVKILRPD 660
 DB 601 prydfrsrslrefekgeqgfgevhlcvdspdpdlyslldplvnrkgnplvavkllrpd 660
 QY 661 ATKNAFSLSFRNDFLEKVKIMSLKDPNIRILGLCYVODDPLCMITDYENEDLNQOFLS 720
 DB 661 atknafslsfrndflekvimslkdpnirilglcyvoddplcmityenendlnqofls 720
 QY 721 AHOLEDKAAGAPDGOAAGPTISYPMLELHVAQAQIASGRYLATINFYHRDLATRNCLY 780
 DB 721 aholedekaagapdgoaagptisypmlelhvaagaqiasgrylatinfhrdlatrncl 780
 QY 781 GNFETIKINDFGMSRLVAGDYRVVGRVAVLPRMAMECILMGKTTASDVAFCVTLM 840
 DB 781 gnfetikiadfgmsrlyagdyrvvgrvavlprrmamecilmgkttasdvafcvtlw 840

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QY 841 EYVLMCRAPFGQLTDEQVYENAGEFFRDGROYLSRPPACPOGLYEIMLCWMSRESE 900
DB 841 EVMLICRAQPIGQLTDEQVYENAGEFFRDGROYLSRPPACPOGLYEIMLCWMSRESE 900
QY 901 RPPFSQHLRFLEADALNTV 919
DB 901 RPPFSQHLRFLEADALNTV 919

RESULT 4
AAR71100
ID AAR71100 standard; Protein: 914 AA.
XX
AC AAR71100;
XX
DT 17-AUG-1995 (first entry)
XX
DE Protein-tyrosine-kinase PTK22.
XX
KM Protein-tyrosine-kinase; PTK; discoidin domain receptor; cancer;
KM breast tumor; mamma carcinoma; diagnosis; prognosis; therapy.
XX
OS Homo sapiens.
XX
PN M09502187-A.
XX
PD 19-JAN-1995.
XX
PF 08-JUL-1994; 94MO-GB01480.
XX
PR 09-JUL-1993; 93GB-0014271.
XX
PA (CANC-) CANCER RES INST.
PA (WELL) WELLCOME FOUND LTD.
XX
PI Barker KT, Crompton MR, Gusterson BA, Martindale JE;
PI Mitchell PJ, Page MJ, Spence P;
PI
DR WPI: 1995-066991/09.
XX
DR N-PSDB; AA084782.
XX
PT Method for screening substances, using protein tyrosine kinase -
PT for potential utility as therapeutic agents for cancer
XX
PS Disclosure: Page 26-30; 51pp. English.
XX
CC cDNA derived from tumor metastatic tissue was amplified using
CC primers (given in AA084783-84) based on sequences (AAR71101, AAR71103)
CC associated with protein-tyrosine-kinases (PTK). Novel PTK22 was
CC identified in an isolated subclone. The 3' sequence of PTK22 was
CC obtained by reverse transcription (using the primer of AA084786) and
CC PCR amplification (primers AA084787-88) of RNA of human breast
CC carcinoma cell line MDA MG 468. The partial DNA sequence of PTK22
CC is given in AA084782.
XX
SQ Sequence 914 AA:

```

```

QY 181 ELYGCLWRBDGLSTAPVGTMTLSEANTYLNDSITDGHVGLQYGGCLADGVGLDD 240
DB 181 ELYGCLWRBDGLSTAPVGTMTLSEANTYLNDSITDGHVGLQYGGCLADGVGLDD 240
QY 241 FRKSOELRWMPGYDYVGVNSHSSFGYEMEEEDRLRAPAMOVHONMHTGARRLPG 300
DB 241 FRKSOELRWMPGYDYVGVNSHSSFGYEMEEEDRLRAPAMOVHONMHTGARRLPG 300
QY 301 VECFRFRGAPAMWEGEPHRLHGNLGDPRARAVSVPLGGRVAFRLQCFLEAPWILFS 360
DB 301 VECFRFRGAPAMWEGEPHRLHGNLGDPRARAVSVPLGGRVAFRLQCFLEAPWILFS 360
QY 361 EISFISDVVNNSSPALGCTFPAPWMPGPPTNFSLELRQO -OPVAKESGPTAIL 419
DB 361 EISFISDVVNNSSPALGCTFPAPWMPGPPTNFSLELRQO -OPVAKESGPTAIL 419
QY 420 IGCIVATIIILLIATLMLRHLRRLSKARVLEBELVHLSVPGDITLNNRGP 479
DB 420 IGCIVATIIILLIATLMLRHLRRLSKARVLEBELVHLSVPGDITLNNRGP 479
QY 480 EPPYOEPRRGNPNSAPCVPNGSALLSNPARYRLATYARPRGPTPAMAKPTN 539
DB 480 EPPYOEPRRGNPNSAPCVPNGSALLSNPARYRLATYARPRGPTPAMAKPTN 539
QY 540 TOAVSGDTMEPEKPGAPLLPFPQNSVPHVAEADIVTLQVGTGNTYAVPALPGAVDG 599
DB 540 TOAVSGDTMEPEKPGAPLLPFPQNSVPHVAEADIVTLQVGTGNTYAVPALPGAVDG 599
QY 541 TQAVSGDTMEPEKPGAPLLPFPQNSVPHVAEADIVTLQVGTGNTYAVPALPGAVDG 600
DB 541 TQAVSGDTMEPEKPGAPLLPFPQNSVPHVAEADIVTLQVGTGNTYAVPALPGAVDG 600
QY 600 PPRVDFPRSRRLREKKEGEGFGEVHCEVDSQDDVSLDFPLNVRKGHLVAVKILRP 659
DB 600 PPRVDFPRSRRLREKKEGEGFGEVHCEVDSQDDVSLDFPLNVRKGHLVAVKILRP 659
QY 601 PPRVDFPRSRRLREKKEGEGFGEVHCEVDSQDDVSLDFPLNVRKGHLVAVKILRP 660
DB 601 PPRVDFPRSRRLREKKEGEGFGEVHCEVDSQDDVSLDFPLNVRKGHLVAVKILRP 660
QY 660 DATKNAFSLSFRNDFLEKVKINSRLKDPNIRLLGYCVDODPLCMCTDYNENGDLNOFL 719
DB 660 DATKNAFSLSFRNDFLEKVKINSRLKDPNIRLLGYCVDODPLCMCTDYNENGDLNOFL 719
QY 661 DATKNAFSLSFRNDFLEKVKINSRLKDPNIRLLGYCVDODPLCMCTDYNENGDLNOFL 714
DB 661 DATKNAFSLSFRNDFLEKVKINSRLKDPNIRLLGYCVDODPLCMCTDYNENGDLNOFL 714
QY 720 SAHOLEDKAABGAPDGOAAGPTISYPMLLHVAQAQIASGMRYLATLNFYHRLAARNC 779
DB 720 SAHOLEDKAABGAPDGOAAGPTISYPMLLHVAQAQIASGMRYLATLNFYHRLAARNC 779
QY 715 SAHOLEDKAABGAPDGOAAGPTISYPMLLHVAQAQIASGMRYLATLNFYHRLAARNC 774
DB 715 SAHOLEDKAABGAPDGOAAGPTISYPMLLHVAQAQIASGMRYLATLNFYHRLAARNC 774
QY 780 VGENFTIKINDFGSRNLVAGDYRVGRVAPLPRKMAACILMGKTTASDVWAGVYL 839
DB 780 VGENFTIKINDFGSRNLVAGDYRVGRVAPLPRKMAACILMGKTTASDVWAGVYL 839
QY 775 VGENFTIKINDFGSRNLVAGDYRVGRVAPLPRKMAACILMGKTTASDVWAGVYL 834
DB 775 VGENFTIKINDFGSRNLVAGDYRVGRVAPLPRKMAACILMGKTTASDVWAGVYL 834
QY 840 WEYVLMCRAPFGQLTDEQVYENAGEFFRDGROYLSRPPACPOGLYEIMLCWMSRESE 899
DB 840 WEYVLMCRAPFGQLTDEQVYENAGEFFRDGROYLSRPPACPOGLYEIMLCWMSRESE 899
QY 900 QRPFSQHLRFLEADALNTV 919
DB 900 QRPFSQHLRFLEADALNTV 919

RESULT 5
AAM34673
ID AAM34673 standard; Protein: 882 AA.
XX
AC AAM34673;
XX
DT 17-FEB-1998 (first entry)
XX
DE Human mammary carcinoma kinase 10 (MCK-10) splice variant 1.
XX
KM Mammary carcinoma kinase; MCK-10; receptor tyrosine kinase;
KM proliferative disease; cancer; insulin receptor family;
KM tyrosine kinase neurotrophin receptor; MCK-10 activity;
KM neurological disorder; aberrant expression.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..18

```

FT Protein /label= signal_sequence
FT 19..919 /note= "mature_protein"
FT 31..185 /label= DiscoIdin_I_like_domain
FT 304..307 /label= DiscoIdin_I_like_domain
FT Cleavage-site /label= endopeptidase_furin
FT /note= "putative precursor cleavage site"
FT 48..439 /label= transmembrane_region
FT Binding-site /label= ATP_binding_motif
FT 765..766 /label= autophosphorylation_sites
FT /note= "putative"
FT Modified-site /label= autophosphorylation_site
FT /note= "putative"
FT Binding-site /label= binding_motif_for_P13_kinase
FT /note= "binding motif for phosphatidylinositol 3' kinase"
FT 807..810 /label= potential_substrate_binding_site
FT 795..795 /label= potential_substrate_binding_site
FT 26..42 /note= "antibody recognition sequence N1alpha"
FT 309..321 /note= "antibody recognition sequence N1beta"
FT 865..882 /note= "antibody recognition sequence C1beta"
FT Region
FT US677144.A.
FT 14-OCT-1997.
FT 08-NOV-1994; 94US-0336343.
FT 16-NOV-1993; 93US-0153397.
FT (ALVE/) ALVES F H E.
FT (ULR/) ULRICH A.
FT Alve FHE; ULRich A;
FT WPI; 1997-511869/47.
FT Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding
FT for it, useful for cancer diagnosis
FT
FT Disclousure; Page -; 70pp; English.
XX The present sequence represents a splice variant of a mammary
CC carcinoma kinase (MCK-10). This kinase belongs to a novel family
CC of receptor tyrosine kinases, and expression is associated with
CC proliferative diseases such as cancer. The MCK-10 receptor tyrosine
CC kinase has extensive sequence similarity to the insulin receptor family.
CC The MCK-10 gene was isolated by PCR using 2 degenerate oligonucleotide
CC primer pools, using a template cDNA synthesised by reverse transcription
CC of poly-A RNA from the human mammary carcinoma cell line MCF7. The
CC amplified PCR product was used to screen human foetal brain and
CC placental libraries, from which the present splice variant was isolated.
CC This splice variant does not possess amino acids 505-541 of MCK-10
CC (AAW3672). The sequence represented by amino acids 548-558 may be
CC important, as deletion of this motif in the activin receptor
CC serine/threonine kinase results in reduced ligand binding affinity.
CC MCK-10 is expressed in brain tissue, and the protein shares homology with
CC the tyrosine kinase neurotrophin receptor. Modulation of MCK-10 activity
CC therefore may be used for treatment of neurological disorders. MCK-10 is
CC also expressed in a variety of cancer cell lines and tumour tissue. The
CC nucleotide sequence of MCK-10, or parts of it, can be used for diagnostic
CC purposes to detect aberrant expression of MCK-10 genes. Inhibitors of
CC MCK-10 (or splice variants) receptor activity may have therapeutic value
CC in the treatment of diseases such as cancer.

CC note: the present sequence does not appear in the specification, but was
CC created using information provided.
XX
XX Sequence 882 AA:
Query Match 95.3%; Score 4697.5; DB 18; Length 882;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 882; Conservative 0; Mismatches 0; Indels 37; Gaps 1;
QY 1 MGPEALSSLLLLLVASGDADKKGHPDPAKCYALGMDRTIPDSDISASSSSDSTAR 60
Db 1 mgealsslllllvassgdadmkgfhdpakcylagmdrtlpsdissasssdsstar 60
QY HSRLESSDGDGKMPAGVFPPEEEXLVQDRLVAVLVGOGHAGGLGFEFSRYRL 120
Db hsrlessdgdgkmpagvfppeexlvqdvrlhvalvgqgnaaglgfestsryrl 120
QY 121 RYSRDGRMMGMDKRWGEVJSGNEDPBGVYLKDGPPMVARLVFYPRADVMSCLRV 180
Db 121 rysrdgrmmgmdkrdwgevjsgnedpbgvylkdgppmvarylvyfyradvmsclrv 180
QY 181 ELYGCLMRDGLSTYAPVQTMVISEAVYLVNDSTYDGHITVGGLOVGGQLADVYGLDD 240
Db 181 elygcclmrdblstyapvqtmviseavylvndstydghtvvglgvgysgladvgvyldd 240
QY 241 FRKSOELRVMPGVDYVGNSNSFSGTYEMEPEFRLAFOVMQVHCNMHTLGRLLPG 300
Db 241 frksaelrvmpgydyvgnsnfsstyemefefrlafqamqvcnmhtlgrllpg 300
QY 301 VECRRRRGPMAMWEGEPNRHNLGNIAGDPARAASVPLGGRVARELOCREFAGPMLFS 360
Db 301 vecrrrrgpmawegepnrhnlgnlgdpraravsvplggrvarelocrflfagpmlfs 360
QY 361 EISFISDVVNNSSPALGTFPPAPMPWPBPPTNSSLLEPRGQPPAKAGSTALLI 420
Db 361 eistfisdvvnsspalgltfppapmpwpbpptnsslleprgqpakagstalll 420
QY 421 GCLVAIIILLLLIILMLMRLHWRRLSKAEERVVEELTVHLSVSGTILINNNPRE 480
Db 421 gclvailllllllmlmrlhwrllskaervvveeltvhlsvsgtillnnnpree 480
QY 481 PPVQEPFRGNPNPHSAPCVNPSSALLSNPAYRULLATYARPPGPPPMAMAKPNT 540
Db 481 ppyqepfrgpnphsacvpnpssallsnpayrullatyarppgpppmamakpnt 540
QY 541 QAYSGDYHEPFRGAPLLPPPPONSVPVRYAEDVTTLOGVTGGNTYVAPLPAGVCGP 600
Db 541 qaysgdyhepfrgappllpppponsvpryiaedvttlogvtggntyvaplpagvcgp 600
QY 601 PRVDFPRRLRFKFKLGSGGGEVHLCEVDSPODVLSDPFLNVRKGGHLLVAVKILRPD 660
Db 601 prvdfprrlrfkfklgsgggevhlcdevdspodvlsdpflnvrkghllvavkrlrpd 660
QY 661 ATKNAFSELSFRNDFLEKVKIMSRLKDPNIRLGLVCVQDDPLCATIDYMEGDLNPLS 720
Db 661 atknafselsfrndflekvikmsrlkdpnirllglvcvqddplcmctdymengdlnpls 720
QY 721 AHQLEDKRAEAPDGGQAAGPTISYPLLVAAQIAGSMYLATLNVHVDLATKCLV 780
Db 721 ahqledkraeapdggqaagptisypmlhvaqiaagmylatlnvhvdlatrclv 780
QY 781 GENTTIKADGSMRNLYAGDYRROGAVPIRMAAMECTLMGFTASVMAFGVTLW 840
Db 781 genttikadgsmrnlyagdyrrrogavpirmaamectlmgftasvmafgvtlw 840
QY 841 EVLMICRAOPGQLTDEQVINEAGEFFRDGROYLSRPPACPGGLYELMRCMSRESEQ 900
Db 841 evlmicraopgqltdeqvineageffrdgroylsrppacpgglyelmrmsreseq 900
QY 901 RPPESQHLRFIAEDALNTV 919
Db 901 rppesqhlrflaedalntv 919
QY 864 IPIFSQHLRFLAEDALNTV 882

AAW34675	6
ID AAW34675	standard; Protein; 876 AA.
XX	
AC AAW34675;	
XX	
DT 17-FEB-1998	(first entry)
XX	
DE Human mammary carcinoma kinase 10 (MCK-10) splice variant 3.	
XX	
KW Mammary carcinoma kinase; MCK-10; receptor tyrosine kinase;	
KW Proliferative disease; cancer; insulin receptor family;	
KM Tyrosine kinase neurotrophin receptor; MCK-10 activity;	
KM neurological disorder; aberrant expression.	
XX	
OS Homo sapiens.	
XX	
FH Key	Location/Qualifiers
FT Peptide	1..18
FT	/label= signal_sequence
FT Protein	19..876
FT	/note= "mature_protein"
FT Domain	31..185
FT	/label= Discoidin_I-like_domain
FT Cleavage-site	304...307
FT	/label= endopeptidase_furin
FT Region	/note= "putative precursor cleavage site"
FT	48..439
FT Binding-site	/label= transmembrane_region
FT	580...590
FT Modified-site	/label= ATP_binding_motif
FT	760...761
FT	/label= autophosphorylation_sites
FT Modified-site	/note= "putative"
FT	756...756
FT	/label= autophosphorylation_site
FT	/note= "putative"
FT Binding-site	802...805
FT	/label= binding_motif_for_PI3_kinase
FT	/note= "binding motif for phosphatidylinositol 3'
FT	kinase"
FT Binding-site	790
FT	/label= potential_substrate_binding_site
FT Region	26...42
FT	/note= "antibody recognition sequence Nterminal"
FT Region	309...321
FT	/note= "antibody recognition sequence Nbeta"
FT Region	860...877
FT	/note= "antibody recognition sequence Cbeta"
XX	
PN US5677144-A.	
XX	
PD 14-OCT-1997.	
XX	
PF 08-NOV-1994;	94US-0336343.
XX	
PR 16-NOV-1993;	93US-0153397.
XX	
PA (ALVE/) ALVES F H E.	
PA (ULLR/) ULLRICH A.	
PI Alves FHE, Ullrich A;	
XX	
DR WPI: 1997-511869/47.	
XX	
PT Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding	
PT for it, useful for cancer diagnosis	
XX	
PS Disclosure; Page -: 70pp; English.	
XX	
CC The present sequence represents a splice variant of a mammary	

CC carcinoma kinase (MCK-10). This kinase belongs to a novel family
CC of receptor tyrosine kinases, and expression is associated with
CC proliferative diseases such as cancer. The MCK-10 receptor tyrosine
CC kinase has extensive sequence similarity to the insulin receptor family.
CC The MCK-10 gene was isolated by PCR using 2 degenerate oligonucleotide
CC primer pools, using a template cDNA synthesized by reverse transcription
CC of poly-A RNA from the human mammary carcinoma cell line MCF7. The
CC amplified PCR product was used to screen human foetal brain and
CC placental libraries, from which the present splice variant was isolated.
CC This splice variant does not possess amino acids 505-541 or 666-671 of
CC MCK-10 (AM33672). The sequence represented by amino acids 548-558 may
CC be important, as deletion of this motif in the activin receptor
CC serine/threonine kinase results in reduced ligand binding affinity.
CC MCK-10 is expressed in brain tissue, and the protein shares homology
CC with the tyrosine kinase neurotrophin receptor. Modulation of MCK-10
CC activity therefore may be used for treatment of neurological disorders.
CC MCK-10 is also expressed in a variety of cancer cell lines and tumour
CC tissue. The nucleotide sequence of MCK-10, or parts of it, can be used
CC for diagnostic purposes to detect aberrant expression of MCK-10 genes.
CC Inhibitors of MCK-10 (or splice variants) receptor activity may have
CC therapeutic value in the treatment of diseases such as cancer.
CC note: the present sequence does not appear in the specification, but was
CC created using information provided.

Query Match	94.5%	Score 4656.5	DB 18	Length 876
Best Local Similarity	95.3%	Pred. No. 0		
Matches 876; Conservative	0	Mismatches	0	Indels 43; Gaps 2;

QY	1	MGPEALSLILLILLVAVSGADKKHEDPAKCRKRYALGMQDSTIDSDISASSMSNSOSTAAR	60
Dd	1	mppeaalslllllllvaagdaamkghfopakcraylqmqdrlfpdsdlssasswsdstaar	60
QY	61	HSRLSSDGDGAWCPAGSVYFPEKEEYTLQVLDQRHLHLVALGTGGRAGIGKREFSRYL	120
Dd	61	hslrleesddgagwcpagsvfpekeeylqvldqrlhlhlvalvgtrnagglgkrefarsryl	120
QY	121	RSRBDGRFMMGKKDRRGQGVISGNNDPBGVYLKDLGPRMVALRYRYPRADRYMSYCLRV	180
Dd	121	rsyrdgrfrmmgwkdrtwgggevslnqnedpegvylkdlgprmmvalryrypradrymsvclrv	180
QY	181	ELVGCMLRBDGLSTYAPVQOTWYLSSEAYLLSDSYDCHTGVGLQYGLGQLADGVVGLDD	240
Dd	181	elvgclwrdglstypavqotwylsseayllsdsydchtgvglqyglgqladgvvgldd	240
QY	241	FRKSQELRWPGYDYGVSNNHSFSSGYYEMFEFEDRLRAQAMQVHCNNMHTLGARLPDG	300
Dd	241	frksqelrwpgydygvsnhsfssgyyemfeffedrlraqamqvhcnnmhtlgarlpdg	300
QY	301	VECRFRGPGAMMEGEPKMHNLGSLGPRARAASVYLGGRVAFQCFELPAGWLLFS	360
Dd	301	vecfrfrgpgammegpkmhnlgsllgpraraasvylggrvafqcfelpagwllfs	360
QY	361	ELSFIFIDVYNNSSPALGCTFPPAHPWPMPGPPPTNFSLELEPPGQOPVAKAEGSPITALI	420
Dd	361	elsfifidvynsspalgctfppahpwpmpgppptnfsleleppgqopvakaegspitali	420
QY	421	GCYVALILLILLIILMLRLMRLMRRLSKAERVALLEELVHLVSYGVDIILNNBPGR	480
Dd	421	gcylvalilllllllmlrlmrlmrllskarervalleelvhlsyvgdillnnbpgr	480
QY	481	PPPYQDPRRGKPPPSAPCVNCSALLNSNPAYRLLIATYARPPRGCPPPAPMAKPPNT	540
Dd	481	pppyqdprrrgkpppsapcvnpnsallnsnpayrlliatyarprrgcpppapmakppnt	540
QY	541	QAVSGCYMPEKEPGAPLPPPPONSYPHYAEDIVTLGGTWGNNYAVPAPLPGAVGDP	600
Dd	505	-aysgcymppekpgapllppppnshyphyaedivtlggtwgnnyavpaplpagvqdp	560
QY	601	PRVDFRSHLRKEKELGSGGFEVHLCEVDSPODLYSLDFPLNVKGRPLLVAYKLRPD	660

Db 564 pvdgfrsrlrfkklgeqgfevhlcevdspqdlvaldfplnvkrkphllvavkllrpd 623
QY 661 ATKAAASRLSRNDPLKEVKIMSLKDPNIRRLIGVCVQDDPLCMITDYMENGDNLQFLS 720
Db 624 atkna-----rnfllkevkmrllkqpnllrllgvcvqddplcmldymengdlnqfls 677
QY 721 AHOEDKAAEGAPDGAAGSPRTISYPMILHVAQAISGMRXYLATLNFVRHDLATRNCLV 780
Db 678 ahqledaaagapdggaagqptlsypmllhvaaglasgmrylatlnfvhrlatrnclv 737
QY 781 GENTTIKADFGMSRNLVAGDYRVQGRAVLPIRMAMECTILMGKFTTASDVMAFGVTLW 840
Db 738 genttlkadtgmernlyagdyrvvgavlpirmamecclngkfttasdvaafgvtlw 797
QY 841 EYLMCLCAQPFQQLTDEQVIENAGEFFRDGROYLISRPACPGYLEMLRCMSRESEQ 900
Db 798 evlmclcrapfgqgtldeqvienegeffrdgroylrsrpacpgglyelmrcwsresed 857
QY 901 RPPSOHLRFLAEDALMTV 919
Db 858 rptsqhlrflaedalnfv 876

RESULT 7
AAB54286
ID AAB54286 standard; Protein: 624 AA.
AC AAB54286;
DT 09-MAR-2001 (first entry)

XX Human pancreatic cancer antigen protein sequence SEQ ID NO:738.
XX
KM Human; Pancreas; pancreatic cancer; pancreatic cancer antigen;
KM detection; diagnosis; identification; cytostatic; neuroprotective;
KM neurotropic; immunomodulatory; relaxant; contraceptive; gynaecological;
KM antinflammatory; cardiant; gene therapy; chromosome mapping;
KM linkage analysis; tissue identification; tissue typing; forensic;
KM neural; immune system; muscular; reproductive; gastrointestinal;
KM pulmonary; cardiovascular; renal; proliferative.
XX
OS Homo sapiens.
XX
PN WO200055320-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000: 2000MO-US05989.
XX
PR 12-MAR-1999: 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-579444/54.
DR N-PSDB; AAC99051.
XX
PT New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition -
XX
PS claim 11; Page 1180-1182; 1379pp; English.
XX
XX AAC98773 to AAC99231 encode the human pancreatic cancer associated
XX proteins, called pancreatic cancer antigens, given in AAB54008 to
XX AAB54466. The human pancreatic cancer antigens have cytostatic,
XX neuroprotective, neurotropic, immunomodulatory, relaxant, contraceptive,
XX gynaecological, cardiant and antinflammatory activities, and can be used
XX in gene therapy. The polynucleotide and proteins can be used for
XX preventing, treating, or ameliorating a medical condition or in assays
XX for diagnosing a pathological condition or a susceptibility to one in a
XX subject. Binding partners to the proteins and the activity of the

CC proteins can be identified. The pancreatic cancer antigens can be used to.
CC detect, treat or prevent pancreatic disorders, especially cancer.
CC Agonists and antagonists to the antigens can be screened for. The
CC pancreatic cancer antigen polynucleotides can be used to design nucleic
CC acid hybridisation probes that can be used in chromosome mapping, linkage
CC analysis, tissue identification and/or typing and a variety of forensic
CC and diagnostic methods. The proteins can be used to generate antibodies
CC which are used to purify, detect and target the polypeptides, including
CC both in vivo and in vitro diagnostic and therapeutic methods. The
CC proteins can be used to treat or prevent neural, immune system, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC sequences used in the exemplification of the present invention.
XX
XX Sequence 624 AA;
SQ

Query Match 66.9%; Score 3298; DB 21; Length 624;
Best Local Similarity 98.7%; Pred. No. 7.7e-245;
Matches 616; Conservative 0; Mismatches 2; Indels 6; Gaps 1;

QY 261 HSFSSGYVMEFEEDRLRPAQAMOVHONNHTLGARLPGVCEFRRGPAWAGEPRRH 320
Db 3 hstssgyvemeffedrlratqamqvhcnmhtlgarlpvgvecfrrgpaawageprmh 62
QY 321 NLGSLNDPPARAAYVPLGGRVAREFLQCRFLFAGPWILFSEISFDVYNNSSPALGTF 380
Db 63 nlgsnlgdpparaavsvplggrvarflqcrflfagpwllfseisfisdvynsspalgltf 122
QY 381 PPAPWMPGPPPTNFSSLELEPRGQOPVAKAEGSPALIGLVAIILLLILALMLMR 440
Db 123 ppapwmpgppptnfssleleprgqpvaekasgspalilgclvaliililalmlwr 182
QY 441 LHMRLSLKARVLEELVHLSVPGDTLILNRPGRPREPPQGEPRRGNPHSAPCV 500
Db 183 lhmrlslkxerryleelvhlsvpgdtlilnrrpgrpreppqgeprpynphsapcv 242
QY 501 PNGSALLSNPARYLLATYARPRGPGPTPAMAKPTNTQAYSGDYMEEKPGAPLLPP 560
Db 243 pngsallsnpaylllatyarprgpgptpamapktntqaysgdymeeekpgapllpp 302
QY 561 PPNQSVPHYAEADIVTLQGYTGCTAVVPALPGCAVDDGPPRVDPPSRLLFKKLCBGQ 620
Db 303 ppnqsvphyaeadivtlqgytgctavvpalpagaavddpprvdfpsrlrfkklgeqg 362
QY 621 FGEVHLCEVDSPODLVSLDPLNVRKGPPLLVAKIIRPATKAAASRLSRNDPLKEVK 680
Db 363 fgevhlcevdspqdlvaldfplnvkrkphllvavkllrpactkna-----rnfllkev 416
QY 681 IMSRLKDPNIRRLIGVCVQDDPLCMITDYMENGDNLQFLSAHOEDKAAEGAPDGAAG 740
Db 417 imsrllkdpnllrllgvcvqddplcmldymengdlnqflsaahqledaaagapdggaag 476
QY 741 GPITISYPMILHVAQAISGMRXYLATLNFVRHDLATRNCLVGENFTTIADFGMSRNLVAG 800
Db 477 gptisypmllhvaaglasgmrylatlnfvhrlatrnclvgenttlkadtgmernlyag 536
QY 801 DYYRVQGRAVLPIRMAMECTILMGKFTTASDVMAFGVTLWELMCLCAQPFQQLTDEQVI 860
Db 537 dyyrvqgravlpirmaamecclngkfttasdvaafgvtlwelmlcrapfgqgtldeqvi 596
QY 861 ENAGEFFRDGROYLISRPACPG 884
Db 597 enageffrdgroylrsrpacpg 620

RESULT 8
AAG73767
ID AAG73767 standard; Protein: 624 AA.
XX
AC AAG73767;
XX
DT 03-SEP-2001 (first entry)

FT	/note- "SHC is an oncogenic SH2 domain containing molecule"
FT	510..513
FT	/label= "GFPase_activity_protein_binding_site
FT	/note- "putative"
FT	26..42
FT	/note- "antibody recognition sequence NTalpha"
FT	309..321
FT	/note- "antibody recognition sequence NDbeta"
FT	897..913
FT	/note- "antibody recognition sequence CTbeta"
XX	
PX	US5671144-A.
PD	
FD	14-OCT-1997.
XX	
FX	08-NOV-1994;
PF	94US-0336343.
PR	
PR	16-NOV-1993;
XX	93US-0153397.
PA	(ALVE/) ALVES F H E.
PA	(ULR/) ULLRICH A.
PI	
PI	Alves FHE, Ullrich A:
DR	
XX	WPI; 1997-511869/47.
PT	
PT	Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding for it, useful for cancer diagnosis
XX	
PS	Disclosure; Page -: 70pp; English.
XX	
CC	The present sequence represents a splice variant of a mammary carcinoma kinase (MCK-10). This kinase belongs to a novel family of receptor tyrosine kinases, and expression is associated with proliferative diseases such as cancer. The MCK-10 receptor tyrosine kinase has extensive sequence similarity to the insulin receptor family. The MCK-10 gene was isolated by PCR using 2 degenerate oligonucleotide primer pools, using a template cDNA synthesised by reverse transcription of polyA RNA from the human mammary carcinoma cell line MCF7. The amplified PCR product was used to screen human foetal brain and Placental libraries, from which the present splice variant was isolated. This splice variant does not possess amino acids 666-671 of MCK-10 (AAW34677). The sequence represented by amino acids 585-595 may be important, as deletion of this motif in the activin receptor- serine/threonine kinase results in reduced ligand binding affinity. MCK-10 is expressed in brain tissue, and the protein shares homology with the tyrosine kinase neurotrophin receptor. Modulation of MCK-10 activity therefore may be used for treatment of neurological disorders. MCK-10 is also expressed in a variety of cancer cell lines and tumour tissue. The nucleotide sequence of MCK-10, or parts of it, can be used for diagnostic purposes to detect aberrant expression of MCK-10 genes. Inhibitors of MCK-10 (or splice variants) receptor activity may have therapeutic value in the treatment of diseases such as cancer. note: the present sequence does not appear in the specification, but was created using information provided.
Sequence	563 AA;

Db	121	lhmtrpgtrepppyqdeprtrpgrnphhsapcwpnsa111snpayr11latyatrppzpppp	180
Qy	531	TPAAKPTNTQAYSGDYMERKPCAPLLPRPPQNSVPHVAEADIYTLQVGTGNTAAVPA	590
Db	181	tpwakrntcaysgdymerkpapq11ppppqnsvphyeadiyltqyrgnucyapra	240
Qy	591	LPRAVGDGPRRVDPFRPSRLRFKKLEGGOFENHLEVDSPDDVSLDPLVNRKCHPL	650
Db	241	lppavsgdpprvdpfrpsr1rfkex1qegqfgevnhleovsdppdlvsldfplnvrxhpl	300
Qy	651	LVAAKILRPDRTKAASSLSFSRNFLEKVRMSLXDPN11RLIGVCVODDPLCMITDYM	710
Db	301	lvaxk11ltpactka-----tnoflvevk1ms11kbpn11fl1gvcvqddp1cm1ctdym	354
Qy	711	ENGDLNOFLSAHQLEDKRAEAGPDDGQAOAGPTTISYMLHLHVAQIASGRYATLNEVH	770
Db	355	engdlnoflshqledkaeaegapddgaaqppctisym1lhvaagdasgmrylatlnfvh	414
Qy	771	RDLATRNCLEVENFTIKIADFGMSRNLVAGDYYRVQGRAVLPIRIMAMECILMGKFTTAS	830
Db	415	rdlatrnc1vgentf1iadfgmsarn1yagdylyvggravlpltrmwec1lmgkfttas	474
Qy	831	DYAAFGYTLMWVYMLCAQAPPGQJLTDQVLEENMAGEFRDDGROYLYSRPACQGLYELM	890
Db	475	dwaafgytlmwv1mlcraqpfgqjltdeqviensagetrigrqy1srpaccqglyelm	534
Qy	891	LRCWSRESEORRPPSOLHRFLAEADALNTV	919
Db	535	lrcwsreseqrrp1sg1hrflaeadalntv	563

	Query Match	Similarity	60-9%	Score	3003	DB	18	Length	563
	Best Local	Similarity	98.9%	Pred.	No.	3.le-22			
	Matches	563	Conservative	0	Mismatches	22	Indels	6	Gaps
QY	351	LFGAPLLESEISFSDVYNNSSPPLAGTFFPAWMPGPPTTFSSLELEPRGOOVAK	410						
Dy	1	lfagpylllseisflsdvynmsspalgctffppapwpppgppttfssllepvyqqpvak	60						
QY	411	AESSPAILIGCLVAIIILLLIITMLMTRLHWRRLSKERRVLEBELTVHLSPGDTI	470						
Dy	61	aegspcaillgcivalllllllslalmrwlhwrrlllskaerylvleelcvhshpydcl	120						
QY	471	LINNRGPREPPPYGEPGRGNPNPSACVCYNGSALLSNAYTLATTAARPPRGDPP	530						

	RESULT	10
CC	AAR75503	
CC	ID	AAR75503 standard; Protein; 855 AA.
XX		
XX	AAR75503;	
XX		
DT	26-NOV-1995	(first entry)
XX		
DE	Human colonic adenocarcinoma kinase 2 (CCK-2).	
XX		
KW	Mammary carcinoma kinase 10; MCK-10; transmembrane receptor; CCK-2;	
RW	receptor tyrosine kinase; colonic adenocarcinoma kinase 2; cancer.	
XX		
OS	Homo sapiens.	
XX		
PN	WO9514088-A.	
XX		
PD	26-MAY-1995.	
XX		
PF	16-NOV-1994; 94MO-EP03797.	
XX		
PR	16-NOV-1993; 93US-0153397.	
XX		
PA	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.	
PI		
PI	Alves FHE, Ullrich A;	
XX		
DR	WPI; 1995-224054/29.	
DR	N-PSDB; MAO92521.	
XX		
PT	New nucleic acid encoding MCK-10 receptor tyrosine kinase - and	
PT	derived vectors, transformed cells, proteins and antibodies useful	
PT	for diagnosis and treatment of proliferative disease, esp. cancer,	
PT	and for screening modulators	
XX		
PS	Disclosure; Page 57-60; 115pp; English.	
XX		
CC	A member of the mammary carcinoal kinase 10 (MCK-10) receptor tyrosine kinase family was identified using a PCR (with two degenerate Oligo primer pools based on conserved sequences of the Kinase domain of receptor tyrosine kinases) and cDNA prepd. from colonic	

CC adenocarcinoma RNA. The nt sequence of the novel receptor,
 CC designated CCK-2, is given in AA092521 and the deduced AA sequence in
 CC AAR75503. Analysis of the CCK-2 nt and AA sequence indicated
 CC significant homology with MCK-10 throughout the extracellular,
 CC transmembrane and intracellular regions. The regions of homology
 CC extend into the N-terminus consensus sequence for the discoidin I
 CC like family of proteins.

XX Sequence 855 AA:

1 Query Match 48.8%; Score 2404; DB 16; Length 855;
 Best Local Similarity 51.8%; Pred. No. 5,7e-176;
 Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

OY 3 PEAISLLILLVAGSDAMKGFDPKARVALGMODRITPBDISASSMSSTAAHS 62
 DB 5 PMLILVILFILPLIS---sakeqvpaicrtylgmsggqipdedltasqwseslaakyg 61
 OY 63 RLESSDGDGAWCPAGSVFPEK-EEYLQVDLQRLHLVALVGTGGRHAGLGKESRSYRLR 121
 DB 62 RIdseegdgawepelprvpeddlkefIdqlhchfItlvgtgrhagngletafamykIn 121
 OY 122 YSRDGRKMGKDRMGQEVISGNEDEGVYLDGPPMAYRLRYEYPRADRYASVCLRYE 181
 DB 122 YSRDGRKMGKDRMGQEVISGNEDEGVYLDGPPMAYRLRYEYPRADRYASVCLRYE 181
 OY 182 YGCLMRQGLLSTAPVGTMTL--SEAVYLDSTYDGHVGTGLOYGGLQGLADGVYGLD 239
 DB 182 YGCLMRQGLLSTAPVGTMTL--SEAVYLDSTYDGHVGTGLOYGGLQGLADGVYGLD 239
 OY 240 DEKRSQELVWPGYDYVGSNHSFSGGYEMEFEFRLAFAQMOYHNNMHTLGRLG 299
 DB 240 DEKRSQELVWPGYDYVGSNHSFSGGYEMEFEFRLAFAQMOYHNNMHTLGRLG 299
 OY 241 dItqchehyvwpgydyvgrnesacngyleImefarItntumkvchnmfakgykItX 300
 DB 241 dItqchehyvwpgydyvgrnesacngyleImefarItntumkvchnmfakgykItX 300
 OY 300 GVECFRRKGPANAMEGEPNRHNLGNTLGDPRARAVSVPLGGRVARELCRFEPALTF 359
 DB 300 GVECFRRKGPANAMEGEPNRHNLGNTLGDPRARAVSVPLGGRVARELCRFEPALTF 359
 OY 301 evqcyf-tseasewepnaIsfplvldvnpasrfvtvphhmasaIkqyhtadwmnf 359
 DB 301 evqcyf-tseasewepnaIsfplvldvnpasrfvtvphhmasaIkqyhtadwmnf 359
 OY 360 SPISITSD-VVNNSSPALGCTFPAPMWPGRPPNFSLELEPRQGVAKAEGSPYAI 418
 DB 360 SPISITSD-VVNNSSPALGCTFPAPMWPGRPPNFSLELEPRQGVAKAEGSPYAI 418
 OY 360 seItIqSdaamyneal---ptsp-----napItYdpmIwvddntrI 400
 DB 360 seItIqSdaamyneal---ptsp-----napItYdpmIwvddntrI 400
 OY 419 IIGCLVAIILLILLITALLMRLHMRRLSKAERYLEELVTHLSVPDITLNNR--P 476
 DB 419 IIGCLVAIILLILLITALLMRLHMRRLSKAERYLEELVTHLSVPDITLNNR--P 476
 OY 401 IIGCLVAIILLILLITALLMRLHMRRLSKAERYLEELVTHLSVPDITLNNR--P 476
 DB 401 IIGCLVAIILLILLITALLMRLHMRRLSKAERYLEELVTHLSVPDITLNNR--P 476
 OY 477 GPREP-----PPYQEPFRGNPNPSABCVPMGSALLLSNPAYRLILATYARP 523
 DB 477 GPREP-----PPYQEPFRGNPNPSABCVPMGSALLLSNPAYRLILATYARP 523
 OY 461 spsegsnstydrIfIrlprdyep-----srllIkIrlpef----- 494
 DB 461 spsegsnstydrIfIrlprdyep-----srllIkIrlpef----- 494
 OY 524 PRGPPPPRPAKKNPTQAVISGDYDEPEKFGAPLPRPPONSVPYHAEADIVTLQGVYTG 583
 DB 524 PRGPPPPRPAKKNPTQAVISGDYDEPEKFGAPLPRPPONSVPYHAEADIVTLQGVYTG 583
 OY 495 -----apgeesegsqvkvkpygspr-----egvphyaedIvnlqgvttg 535
 DB 495 -----apgeesegsqvkvkpygspr-----egvphyaedIvnlqgvttg 535
 OY 584 NTYAVPALPAGVGGPPRY-DEPRSRLEKFKELGSGGEGEYHLCVDSPODLVLSDEFL 642
 DB 584 NTYAVPALPAGVGGPPRY-DEPRSRLEKFKELGSGGEGEYHLCVDSPODLVLSDEFL 642
 OY 536 ntysrpavtmldIsqkdvaaveefprkItfIkexIgeggIgevhIcvegmekfkdIdfai 595
 DB 536 ntysrpavtmldIsqkdvaaveefprkItfIkexIgeggIgevhIcvegmekfkdIdfai 595
 OY 643 NVKRGHPLLVAVKILRPDANKASFLSRLNDELKEVKIMSLKDPNITRLIGVCYQDDP 702
 DB 643 NVKRGHPLLVAVKILRPDANKASFLSRLNDELKEVKIMSLKDPNITRLIGVCYQDDP 702
 OY 703 LCMITDYHENGDLNPLSHOLEDKAEGAPDDGAAGPTISYPMILHVAAOIASGMRY 762
 DB 703 LCMITDYHENGDLNPLSHOLEDKAEGAPDDGAAGPTISYPMILHVAAOIASGMRY 762
 OY 650 lcmIteymengdlngIIshe-----pnussssdvrtvsytulklkImacqIasgmky 700
 DB 650 lcmIteymengdlngIIshe-----pnussssdvrtvsytulklkImacqIasgmky 700
 OY 763 LATLNFVHDLATRNCLVGENFTIKIADGSGRNLYAGYGVVGRNAVPIRMMAECLT 822
 DB 763 LATLNFVHDLATRNCLVGENFTIKIADGSGRNLYAGYGVVGRNAVPIRMMAECLT 822
 OY 701 lsslnfvhndItrncIvgknItkIadgmstnIlysgdyrIlgdvaIpIltwmsswesI 760
 DB 701 lsslnfvhndItrncIvgknItkIadgmstnIlysgdyrIlgdvaIpIltwmsswesI 760
 OY 833 NGKFTASDVMAFGVTLWEVLMLCRAQPPGQLTDEOVLENAGEFFRDOOROVYLSRPPAC 882
 DB 833 NGKFTASDVMAFGVTLWEVLMLCRAQPPGQLTDEOVLENAGEFFRDOOROVYLSRPPAC 882

DB 761 lgtftasdvmafgvltwelftcgeppysqlsdegvientgfeifrdgrtylpqpalc 820
 OY 883 POGILYELMRCWRESEBQRPFSOLHRLAE 913
 DB 821 pdsaykImlscwrdrcknpsfgehlIlliI 851

RESULT 11

AA75505 ID AAR75505 standard; Protein; 855 AA.

AC AAR75505;

XX 26-NOV-1995 (first entry)

DE Human colonic adenocarcinoma kinase 2 (CCK-2).

XX Mammary carcinoma kinase 10; MCK-10; transmembrane receptor; CCK-2;

KW receptor tyrosine kinase; colonic adenocarcinoma kinase 2.

OS Homo sapiens.

PN WO9514089-A.

XX 26-MAY-1995.

PF 16-NOV-1994; 94WO-EP03799.

XX 16-NOV-1993; 93US-0153397.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Alves FHE, Ullrich A;

DR WPI; 1995-22405/29.

XX N-PSDB; AA092523.

PT New nucleic acid encoding CCK-2 receptor tyrosine kinase - and

PT derived vectors, transformed cells, proteins and antibodies, useful

PT for diagnosis and treatment of proliferative and nervous system

PS diseases and for screening modulators

XX Disclosure; Page 74-77; 115pp; English.

CC A member of the mammary carcinoma kinase 10 (MCK-10) receptor
 CC tyrosine kinase family was identified using a PCR (with two
 CC degenerate oligo primer pools based on conserved sequences of the
 CC kinase domains of receptor tyrosine kinases) and cDNA prep. from
 CC colonic adenocarcinoma RNA. The nt sequence of the novel receptor,
 CC designated CCK-2, is given in AA092523 and the deduced AA sequence in
 CC AAR75503. Analysis of CCK-2 nt and AA sequences indicated significant
 CC homology with MCK-10 throughout the extracellular, transmembrane
 CC and intracellular regions. The regions of homology extend into the
 CC N-terminus consensus sequence for the discoidin I like family of
 CC proteins. CCK-2 was predominantly found in all stromal cells
 CC whereas MCK-10 expression was strongly confined to neoplastic
 CC cells themselves. Between the two RTs, the juxtaposition region
 CC is the region of most extensive sequence divergence.

XX Sequence 855 AA:

1 Query Match 48.8%; Score 2404; DB 16; Length 855;
 Best Local Similarity 51.8%; Pred. No. 5,7e-176;
 Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

OY 3 PEAISLLILLVAGSDAMKGFDPKARVALGMODRITPBDISASSMSSTAAHS 62
 DB 5 PMLILVILFILPLIS---sakeqvpaicrtylgmsggqipdedltasqwseslaakyg 61
 OY 63 RLESSDGDGAWCPAGSVFPEK-EEYLQVDLQRLHLVALVGTGGRHAGLGKESRSYRLR 121
 DB 62 RIdseegdgawepelprvpeddlkefIdqlhchfItlvgtgrhagngletafamykIn 121
 OY 122 YSRDGRKMGKDRMGQEVISGNEDEGVYLDGPPMAYRLRYEYPRADRYASVCLRYE 181
 DB 122 YSRDGRKMGKDRMGQEVISGNEDEGVYLDGPPMAYRLRYEYPRADRYASVCLRYE 181
 OY 182 YGCLMRQGLLSTAPVGTMTL--SEAVYLDSTYDGHVGTGLOYGGLQGLADGVYGLD 239
 DB 182 YGCLMRQGLLSTAPVGTMTL--SEAVYLDSTYDGHVGTGLOYGGLQGLADGVYGLD 239
 OY 240 DEKRSQELVWPGYDYVGSNHSFSGGYEMEFEFRLAFAQMOYHNNMHTLGRLG 299
 DB 240 DEKRSQELVWPGYDYVGSNHSFSGGYEMEFEFRLAFAQMOYHNNMHTLGRLG 299
 OY 241 dItqchehyvwpgydyvgrnesacngyleImefarItntumkvchnmfakgykItX 300
 DB 241 dItqchehyvwpgydyvgrnesacngyleImefarItntumkvchnmfakgykItX 300
 OY 300 GVECFRRKGPANAMEGEPNRHNLGNTLGDPRARAVSVPLGGRVARELCRFEPALTF 359
 DB 300 GVECFRRKGPANAMEGEPNRHNLGNTLGDPRARAVSVPLGGRVARELCRFEPALTF 359
 OY 301 evqcyf-tseasewepnaIsfplvldvnpasrfvtvphhmasaIkqyhtadwmnf 359
 DB 301 evqcyf-tseasewepnaIsfplvldvnpasrfvtvphhmasaIkqyhtadwmnf 359
 OY 360 SPISITSD-VVNNSSPALGCTFPAPMWPGRPPNFSLELEPRQGVAKAEGSPYAI 418
 DB 360 SPISITSD-VVNNSSPALGCTFPAPMWPGRPPNFSLELEPRQGVAKAEGSPYAI 418
 OY 360 seItIqSdaamyneal---ptsp-----napItYdpmIwvddntrI 400
 DB 360 seItIqSdaamyneal---ptsp-----napItYdpmIwvddntrI 400
 OY 419 IIGCLVAIILLILLITALLMRLHMRRLSKAERYLEELVTHLSVPDITLNNR--P 476
 DB 419 IIGCLVAIILLILLITALLMRLHMRRLSKAERYLEELVTHLSVPDITLNNR--P 476
 OY 401 IIGCLVAIILLILLITALLMRLHMRRLSKAERYLEELVTHLSVPDITLNNR--P 476
 DB 401 IIGCLVAIILLILLITALLMRLHMRRLSKAERYLEELVTHLSVPDITLNNR--P 476
 OY 477 GPREP-----PPYQEPFRGNPNPSABCVPMGSALLLSNPAYRLILATYARP 523
 DB 477 GPREP-----PPYQEPFRGNPNPSABCVPMGSALLLSNPAYRLILATYARP 523
 OY 461 spsegsnstydrIfIrlprdyep-----srllIkIrlpef----- 494
 DB 461 spsegsnstydrIfIrlprdyep-----srllIkIrlpef----- 494
 OY 524 PRGPPPPRPAKKNPTQAVISGDYDEPEKFGAPLPRPPONSVPYHAEADIVTLQGVYTG 583
 DB 524 PRGPPPPRPAKKNPTQAVISGDYDEPEKFGAPLPRPPONSVPYHAEADIVTLQGVYTG 583
 OY 495 -----apgeesegsqvkvkpygspr-----egvphyaedIvnlqgvttg 535
 DB 495 -----apgeesegsqvkvkpygspr-----egvphyaedIvnlqgvttg 535
 OY 584 NTYAVPALPAGVGGPPRY-DEPRSRLEKFKELGSGGEGEYHLCVDSPODLVLSDEFL 642
 DB 584 NTYAVPALPAGVGGPPRY-DEPRSRLEKFKELGSGGEGEYHLCVDSPODLVLSDEFL 642
 OY 536 ntysrpavtmldIsqkdvaaveefprkItfIkexIgeggIgevhIcvegmekfkdIdfai 595
 DB 536 ntysrpavtmldIsqkdvaaveefprkItfIkexIgeggIgevhIcvegmekfkdIdfai 595
 OY 643 NVKRGHPLLVAVKILRPDANKASFLSRLNDELKEVKIMSLKDPNITRLIGVCYQDDP 702
 DB 643 NVKRGHPLLVAVKILRPDANKASFLSRLNDELKEVKIMSLKDPNITRLIGVCYQDDP 702
 OY 703 LCMITDYHENGDLNPLSHOLEDKAEGAPDDGAAGPTISYPMILHVAAOIASGMRY 762
 DB 703 LCMITDYHENGDLNPLSHOLEDKAEGAPDDGAAGPTISYPMILHVAAOIASGMRY 762
 OY 650 lcmIteymengdlngIIshe-----pnussssdvrtvsytulklkImacqIasgmky 700
 DB 650 lcmIteymengdlngIIshe-----pnussssdvrtvsytulklkImacqIasgmky 700
 OY 763 LATLNFVHDLATRNCLVGENFTIKIADGSGRNLYAGYGVVGRNAVPIRMMAECLT 822
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 OY 701 lsslnfvhndItrncIvgknItkIadgmstnIlysgdyrIlgdvaIpIltwmsswesI 760
 DB 701 lsslnfvhndItrncIvgknItkIadgmstnIlysgdyrIlgdvaIpIltwmsswesI 760
 OY 833 NGKFTASDVMAFGVTLWEVLMLCRAQPPGQLTDEOVLENAGEFFRDOOROVYLSRPPAC 882
 DB 833 NGKFTASDVMAFGVTLWEVLMLCRAQPPGQLTDEOVLENAGEFFRDOOROVYLSRPPAC 882

```

OY 122 YSRDGRNMGWKNRNGOEIVSGNEDPEGVVLKLDGPMAVARLVRFPYPRADRYMSVCLVE 181
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 122 ysrDgrNMGWknRNNGoeIVSGnEDpEGVvLKldGPMAvARLVRfPYPRADrYMSvCLVE 181
OY 182 LYGCLMRDGLSYTPAPVQOTMYL--SEAVYLNDSTYDCHTYGGLQYGLQLADGVGLD 239
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 182 lYgclMRdGLsYtPAPVqOTMYL--SEAVyLNDSTyDCHtYgGLQyGLqLADGVGLD 239
OY 240 DFRKSOELRWPGDYVGMNSHNSFSSGVVEMEPEDRLRAQAQMOVHNNMHTLGAARLP 299
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 241 dfrKSOELrWpGDyVGMNShNSfSSGVvEMePEdRLRAQaQMovHNNMHTLGAARLP 299
OY 300 GVECFRRRGPMAWEGEPMRNHNLGNTLDPARAAVSYPVLGGRVAFLOCRFLFAPMLLF 359
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 301 evGcyf-rSeasewepnaIsfPlMldvnpaIsfvtYpLhRmasaIkcgYhIdctwmf 359
OY 360 SEISFISP-VYNNSSPALGCTFPAPPMWPPGPPPTNFSLELEPRGQOPVAKAGSPTAI 418
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 360 seIfgsdaaYnnseal---plsp-----maptydpmIkvdnsrtrI 400
OY 419 LIGCLVAIIILLTLIALMLRLLRLLSKAERVLLEELTVHLSVPGDILNNR--P 476
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 401 lIgclvaIfIILlTLiAlMLrLLRlLlSkAeRvLLEeLTVhLSvPGdILNNR--P 476
OY 477 GPRRP-----PRYQEPFRGNPPHSAPCVPNGSALLSNPAYRLILATYARP 523
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 461 spSeqgsnStYdrIfPlrPydEp-----srIlrkIpef----- 494
OY 524 PRGPGPPTPAAKPTNTNOAVSGDMEPEKPGAPILPPRPNQSVPHVLAEDVTLQGVTCG 583
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Db 495 -----apgeesegsgvYkPvqpsp-----egYpHyaeadIvnlqYvtg 535
OY 584 NTYAVPALPRGAVDGPFRV-DEPRSRIRKREKLEGEQFGEVHLCEYDSDODLSLDEPL 642
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 536 nTyavpavtmdIlsgkdvaveefrKlItfKekIgeqgfgeVhLceVegmekfKdkfal 595
OY 643 NVKRGHLLVAVKILRPDARKNAFSFLSRNDLKEVKIKSRLKDPNIIRLLGCVYDDP 702
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 596 dVaangpVlYaVknLrAdakna-----rndfIkElkImSrIkdpIlhIsvcltdp 649
OY 703 ICMITDYMENGDLNOFLSAHOLDKAEGAPRGQAAGSTISYPMILHRAQIASGMRY 762
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 650 lCmItEymengdLnqfIsrHe-----pRnsasdvItvaytLnKlmatqIasgmY 700
OY 763 LATLNFVHRDLATRNCLVGENFTIKIADFGMSHNLAYAGDYRVGRVLPFRMMANECIL 822
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 701 lSaLnfVhrdLatRNclVgEnftIKIAdFGmsHnLayAGdyRVgRvLPFRmMAnECIL 760
OY 823 MGFETIASDYWAFGVTLMLEYLMCRAPFGQLTDEQVIENAGEFFRDQGRQVYLSRPPAC 882
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 761 lGkftIasdyWafGvTlMeylMCRaPFGqLTDegvIENaGEFFRDQGRQvYLSrPPaC 820
OY 883 PGLYELMLRCWRSRSEORPPFSQLRFLAE 913
    |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 821 pGlyElMLrCWrsRSeORppFSqLrFLAE 851

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FH Key Location/Qualifiers
FT Modified-site 121
FT FT /note- "N-glycosylated"
FT Modified-site 213
FT FT /note- "N-glycosylated"
FT Modified-site 261
FT FT /note- "N-glycosylated"
FT Modified-site 280
FT FT /note- "N-glycosylated"
FT Modified-site 328
FT FT /note- "N-glycosylated"
FT Modified-site 372
FT FT /note- "N-glycosylated"
FT Modified-site 503
FT FT /note- "putative autophosphorylation and substrate binding site"
FT Modified-site 736
FT FT /note- "putative autophosphorylation and substrate binding site"
FT Modified-site 740
FT FT /note- "putative autophosphorylation and substrate binding site"
FT Modified-site 741
FT FT /note- "putative autophosphorylation and substrate binding site"
FT Modified-site 813
FT FT /note- "putative autophosphorylation and substrate binding site"
FT Modified-site 825
FT FT /note- "putative autophosphorylation and substrate binding site"
FT Region 400..421
FT FT /label- "transmembrane-region"
FT FT /note- "putative"
FT Domain 30..185
FT FT /label- "DiscoIdn_1-like_domain"
FT Binding-site 433..438
FT FT /label- "protein_kinase_C_binding_site"
FT FT /note- "putative"
PN US5677144-A.
PD 14-OCT-1997.
PD XX
PF 08-NOV-1994. 94US-0336343.
PF XX
PR 16-NOV-1993. 93US-0153397.
PR XX
PA (ALVE/) ALVES F H E.
PA (ULNR/) ULLRICH A.
PI Alves FHE, Ullrich A:
XX
XX WPI: 1997-511869/47.
XX DR N-PSDB: AAT93784.
XX
XX Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding
XX PT for it, useful for cancer diagnosis
XX
XX Claim 5; Fig 3; 70pp; English.
XX
XX The present sequence represents the amino acid sequence of human CCK-2,
XX a member of the mammary carcinoma kinase 10 (MCK-10, AAW34672) family of
XX receptor tyrosine kinases. The protein contains a remarkably high
XX number of proline residues arranged as PXXP or PXXXP repeats, suggesting
XX a random coil structure for the hydrophilic juxtamembrane region. This
XX region is probably a major domain for interactions with cellular
XX substrates and other regulatory proteins. Expression of CCK-2 is
XX associated with proliferative diseases such as cancer. The CCK-2 gene
XX was identified by PCR and a cDNA prepared from colonic adenocarcinoma
XX RNA. CCK-2 is expressed in a wide variety of cancer cell lines and
XX tumour tissue. The CCK-2 nucleic acids can be used for diagnostic
XX purposes to detect aberrant expression of CCK-2 genes. Engineered cell
XX

```

CC lines, containing recombinant vectors with the present sequence, are
CC useful for producing infectious retroviral particles. The cell lines may
CC also be used to evaluate and screen drugs involved in CCR-2 activation
CC and regulation.

XX
SQ Sequence 855 AA:

Query Match 48.8%; Score 2404; DB 19; Length 855;
Best Local Similarity 51.8%; Pred. No. 5,7e-176;
Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

```

OY 3 PEALSLILLVLLVSGADMGKGFDPKAKRYALGMODRTIPDSISASSWSSTAAHS 62
DB 5 pmlilvllfillpils---sakeqvpalcryplgmsggqldedltassqwsstaakyg 61
OY 63 RLESDGDGAWCPAGSVFPEK-EEYLVQVDLQRLHLVALVGTGGRHAGLGKESRSYRLR 121
DB 62 rldseegdgawcpelprepddikefildhthlftlvtggrhagghgtetapmykln 121
OY 122 YSRGRRMGKDRMGQEVISGNEDEGVVVKDGLGPPMVALVRFYPRADRVMSVCLAYE 181
DB 122 ysrldgrwswrnthgkqvlidgnanpydflkldleplvarfvrlfpyvdhsmvcmayve 181
OY 182 LYGLMARDGLSTYAPVGOTMYL--SEAVYLNDSTYDGHVVGGLQYGGQLADGVGGLD 239
DB 182 lygcwldglstysnapgqgfvlpqgsillylndsvdyg-avgyamtegiyqldtgvsgld 240
OY 240 DFRSQELRVMPGYDYVGMNHSFSSGVEMEFEDRLRAFOAMQVHCNNMTLBARLPG 299
DB 241 dftqgheyhvwpdydyvgrnesatngylelmfedrlrnfctmkyhcnmhtakvklfx 300
OY 300 GVECRFRGPRAMAGGEMKRNHNLGCLDPRARAVSVPLGGRVARELQCRFLFAGPWLEF 359
DB 301 evqgyf-rseasewepnasifpilydvnpaarfvtvplhmmsaalkcgyhfadctmmf 359
OY 360 SEISFISD-VVNNSSPALGTFPPAPMPWPPPPPNFSSLELPPGQCPVAKABSPRAI 418
DB 360 selftqdaamylnseal-----cpse-----mapctydmklkvdsnrlr 400
OY 419 LIGCLVALIILLIILALMLRMLRRLSKAERVLEELTVHLSVGDFTLLNNR--P 476
DB 401 lllgclvalilllillllyllwrgfwqmklekastriidmentvalspsdsfmfnms 460
OY 477 GPRP-----PRYGPRPRGNPHSPACVPNGSALLSNPAYRILLATYARP 523
DB 461 spseqgsnstydrllfplrpdyep-----srlrlrkipef----- 494
OY 524 PRGPGPTPAMAKPTNTQAVSGDYMPEKPGAPLLPPQNSVPHVYAEADIVTLQGVYTG 583
DB 495 -----apgeegscgsvvkvqpsgp-----egvphyaadlvnlqgyv 535
OY 584 NTYAVPALPGVAGDGPVPR-DEFRSRLRFRKELGEGQFGEVHCEVDSPODLVSLDFPL 642
DB 536 ntyavpavtmdllsgkdvaavefprklltfkexlgeggvhlcevegmekftdkdal 595
OY 643 NVKRGHPLVAVITLRDARKNASFLSRNDPFLKEYKMSRLKDPNITRLLGVCOVDDP 702
DB 596 dvanqgvlyavvknlradekna-----rnfllkeiklmrllkpnllhllsvcltdp 649
OY 703 ICMITIDMENGDNLQFSAHQLEDKAEGAPGCGAAGPPTISYPMILHLVAQAQIASGMRY 762
DB 650 lclmteymengdngfslrte-----ppmsssdvrtvstnllkfnatqlaasgmk 700
OY 763 LATLNFVHRLDARNCILVGENFTIKIADFGMSRNLVAGDYRVGGRVAVLPRWAAWACIL 822
DB 701 lsslnfthrlactncnlvgnytkladfmsnlysgdyrrlqgrvplrtmssesll 760
OY 823 MGEFTASDVWAGCVTLMEVLMCLRAQPFQQLDDEVYENAGFEFFDQAGQVYLSRPPAC 882
DB 761 lgtftclasdavwagvtlweftfcgeqepqysldeqvlentgetfcdqgqctylpqaalc 820
OY 883 PGLYELMLRCMSRESEORPPFSQLHRLFAE 913

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DB 821 pdsyklmscwrtldtknpsfqlhlllg 851

RESULT 13

AAW77114 standard; Protein; 855 AA.

AAW77114;

16-NOV-1998 (first entry)

DiscoIdin domain receptor 2 protein.

DiscoIdin domain receptor; transformation; metastasis; collagen; ss;
Cleidocranial dysplasia; Stickler syndrome; extracellular matrix; MMP-1.

Homo sapiens.

W09834954-A2.

13-AUG-1998.

05-FEB-1998; 98WO-CA00093.

06-FEB-1997; 97US-0041578.

(MOUN) MOUNT SINAI HOSPITAL CORP.

Pawson A, Vogel W;

WPI; 1998-447168/38.

DR N-PSDB; AAV48292.

Novel ligands of discoIdin domain receptor tyrosine kinase,
especially collagen - useful for treating e.g. metastasis,
cleidocranial dysplasia or stickler syndrome

Disclosure; Fig 22a; 115pp; English.

The discoIdin domain receptor (DDR) can be used to identify and evaluate
substances which affect DDR receptor tyrosine kinase signalling pathways
in the cell. Compounds which modulate such signalling pathways can be
used to alter transformation or metastasis in mammals, to treat
conditions involving structural or functional deregulation of collagens,
e.g. cleidocranial dysplasia or Stickler syndrome, conditions requiring
modulation of extracellular matrix synthesis, degradation or remodelling,
or to treat conditions needing modulation of MMP-1 expression such as
wound healing.

Sequence 855 AA;

Query Match 48.8%; Score 2404; DB 19; Length 855;
Best Local Similarity 51.8%; Pred. No. 5,7e-176;
Matches 482; Conservative 118; Mismatches 227; Indels 104; Gaps 16;

```

OY 3 PEALSLILLVLLVSGADMGKGFDPKAKRYALGMODRTIPDSISASSWSSTAAHS 62
DB 5 pmlilvllfillpils---sakeqvpalcryplgmsggqldedltassqwsstaakyg 61
OY 63 RLESDGDGAWCPAGSVFPEK-EEYLVQVDLQRLHLVALVGTGGRHAGLGKESRSYRLR 121
DB 62 rldseegdgawcpelprepddikefildhthlftlvtggrhagghgtetapmykln 121
OY 122 YSRGRRMGKDRMGQEVISGNEDEGVVVKDGLGPPMVALVRFYPRADRVMSVCLAYE 181
DB 122 ysrldgrwswrnthgkqvlidgnanpydflkldleplvarfvrlfpyvdhsmvcmayve 181
OY 182 LYGLMARDGLSTYAPVGOTMYL--SEAVYLNDSTYDGHVVGGLQYGGQLADGVGGLD 239
DB 182 lygcwldglstysnapgqgfvlpqgsillylndsvdyg-avgyamtegiyqldtgvsgld 240

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Db      655 eymengdingfisthepisscsda-----tvsyankkmatqiasgmkyssln 704
OY      768 FVHRLARNCILVGENFTIKIDFGMSRNLYAGDYRVOGRAVLPIRMAMECILMGKPT 827
Db      705 fvhrlarncilvgenftikidfgmsrnlsgdyrigravlpirmmsweslllgkft 764
OY      828 TASDVMAFGVILMEVIMICRAQPFQGLTDEQVLENAGEFFROGROYLISRPACPGILY 887
Db      765 tasdvmafgyilwefitfcgeqpsqdsdeqviengtgeffidqgrqlylpapalpcdsy 824
OY      888 ELMLCWMSRESQRPFPQSOLHRLFLAE 913
Db      825 klmiscwretckhpsfgeihlillq 850

RESULT 15
AAM81409
ID      AAM81409 standard; Protein: 854 AA.
XX
AC      AAM81409;
XX
DT      22-JAN-1999 (first entry)
XX
DE      Receptor protein tyrosine kinase (PTK) subtype tyro-10.
XX
KM      PTK; receptor; protein tyrosine kinase; recombinant; grafting;
XX      diagnosis; tumour; skin transplant; connective tissue; tyro-10.
XX
OS      Rattus sp.
XX
PN      US837448-A.
XX
PD      17-NOV-1998.
XX
PF      02-MAY-1994; 94US-0237401.
XX
PR      15-MAY-1992; 92US-0884486.
XX      02-MAY-1994; 94US-0237401.
PA      (SALK ) SALK INST BIOLOGICAL STUDIES.
PI      Lal CHC, Lemke GE;
XX
XX      WPI, 1999-023436/02.
DR      N-PDOB; AAV65317.
XX
XX      Nucleic acids encoding protein tyrosine kinase subtypes - for
PT      identification of new subtypes and treatment of diseases associated
PT      with the kinase
XX
XX      Claim 10; Columns 53-58; 47pp; English.
XX
XX      This represents a receptor protein tyrosine kinase (PTK) subtype
CC      tyro-10. The invention provides sequences AAV65308 to AAV65313, AAV65315,
CC      and AAV65317 to AAV65319 that encode proteins having a tyrosine kinase
CC      domain and a tissue expression pattern of a receptor PTK subtype selected
CC      from tyro-1, tyro-2, tyro-3, tyro-4, tyro-5, tyro-6, tyro-8, tyro-10,
CC      tyro-11, and tyro-12, respectively. The polynucleotides are useful for
CC      the detection of tyrosine kinase domain sequences and detection of tissue
CC      expression patterns of PTK subtypes. The cDNAs can also be injected into
CC      oocytes, the protein expressed, and expression products screened for
CC      using antibodies against tyrosine kinase epitopes. These subtypes
CC      sequences can be used for the design of oligonucleotides, for use in
CC      amplification reactions to isolate other subtype sequences. These
CC      (receptor) PTKs. Recombinant vectors expressing the subtypes can be used
CC      to treat related diseases e.g. tumours, by introduction of the vectors
CC      into skin transplants, then grafting these into the connective tissue of
CC      the dermis, thus specifically targeting tumours as the proteins are
XX      released from the matrix.
XX
XX      Sequence 854 AA:

```

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Query Match      48.7%; Score 2402; DB 20; Length 854;
Best Local Similarity 51.9%; Pred. No. 8e-176;
Matches 481; Conservative 119; Mismatches 220; Indels 106; Gaps 16;

OY      9 LLLLLIVASGDMDKMGHPDPAKCRALQMODPTIDSDISASSSSNSDSTAAHSHLESDD 68
Db      10 vlllllllllgsa--kaqvpaalcryplgmssghlpdedlaasqssesaakaygrldsee 67
OY      69 GDGAWCPAGSVPEKE-EEYLVDLQRLHVALVVGOGHAGAGLGEFERSRYLRLKRSRGR 127
Db      68 gdaawcpelpvpddlketlqldkrltlltltvgqgrnaggltetapmykinyrds 127
OY      128 RMWGKDRWGQEVISGNEDEPBGVILKDLAPPVAVRLVFFYPADRVMSVCLRELYGCLM 187
Db      128 rtwlswrnrhkgvldgnanpdyfvklleprlvarfvrllypvtshsmvcmvteylgycw 187
OY      188 RDGLLSTYAPVQIMYL--SEAVYLNDSITYDGHVVGILQYGGGLGDLADGVGLDFRRSQ 245
Db      188 ldglysynapagqgfvlp9gsillyndasydg-avgymtegl9qltdgvsqldfdtqth 246
OY      246 ELRWMPGYDYVGMSNHSFSGVEMEFEDRLRAQAOVHONNMHTGALRLPGVECRF 305
Db      247 ehwvpydyvgwmesatnglfeidrltnltknvchnmfakgvkikveqcyf 306
OY      306 RRGPMAMEGEPMRHLNGLDPPARAVSVPLGGRVAFLOCRFLFAGPMLTFSEISFI 365
Db      307 rrsasewepctavfplldvnpaarfvtvplhmrmsalkcyghfdtmmfseitfq 365
OY      366 SD--VYNNSPALGTFPPAPMPWPPGPTNFSSLELEPRGOQVPAKAGSPTALLIGCL 423
Db      366 sdaamyns----galptsp-----maptydpmkvdnsntflllgcl 405
OY      424 VAILLLLLIILALMLRHLWRRLSKARRVLEELTYHLSVPGDTLLINR-----PEPR 479
Db      406 valfillallavllwrfwtkmlkaskrllldemtvtlslpessmfnmrsspsq 465
OY      480 EP-----PPYQEPFRPGNPPHSAFCVNGSALLNSPVRLLATYARPPRPG 528
Db      466 esnstydrilfrlpdygp-----srllrlkpef----- 494
OY      529 PPTPAMAKPTNTQAVSGDYMEPEKGAFLPPPPONSVPHYAADIYTLQGVGTGNTYAV 588
Db      495 -----aggeesgcsgvfkpaqngp-----egvphyaeadiynlgvtgntcyv 540
OY      589 PALPRGAYGDGPPRY-DPPRSRLRKFKELGSGGCEVHLCEVDSBODLVSDFLNARKG 647
Db      541 pavtmdllsgkdvaveefprkllafikekgqfgevhlcvegmekfkdkdaldvsan 600
OY      648 HPLVAVKILRPDATKNASFLSRNDPLKEVKIMSRDKDNTIRLIGCVQODPLCMIT 707
Db      601 qpvlvavvkmrlradankna-----rndllikeklmsrltkdpnllrlllavctedplcmllt 654
OY      708 DYMEGNDINQFLSAHQLEDKAEGAPGDGAAGPTTISYPMILHVAQAIGMRYLATLN 767
Db      655 eymengdingfisthepisscsda-----tvsyankkmatqiasgmkyssln 704
OY      768 FVHRLARNCILVGENFTIKIDFGMSRNLYAGDYRVOGRAVLPIRMAMECILMGKPT 827
Db      705 fvhrlarncilvgenftikidfgmsrnlsgdyrigravlpirmmsweslllgkft 764
OY      828 TASDVMAFGVILMEVIMICRAQPFQGLTDEQVLENAGEFFROGROYLISRPACPGILY 887
Db      765 tasdvmafgyilwefitfcgeqpsqdsdeqviengtgeffidqgrqlylpapalpcdsy 824
OY      888 ELMLCWMSRESQRPFPQSOLHRLFLAE 913
Db      825 klmiscwretckhpsfgeihlillq 850

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Mon Oct 7 15:50:44 2002

Job time: 261 sec

us-08-153-397a-2.rag

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